

RAW SEQUENCE LISTING

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Application Serial Number: 10/593,532
Source: IFWP
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IFWP

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DATE: 09/27/2006

PATENT APPLICATION: US/10/593,532

TIME: 10:17:32

Input Set : A:\Herr-SFEC-00973-05-SEQ.txt

Output Set: N:\CRF4\09272006\J593532.raw

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3 <110> APPLICANT: University of Virginia Patent Foundation
4     Herr, John C.
5     Kim, Young-Hwan
7 <120> TITLE OF INVENTION: SFEC, A Sperm Flagellar Energy Carrier Protein
9 <130> FILE REFERENCE: 00973-05
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/593,532
C--> 11 <141> CURRENT FILING DATE: 2006-09-18
11 <150> PRIOR APPLICATION NUMBER: US 60/554,085
12 <151> PRIOR FILING DATE: 2004-03-17
14 <150> PRIOR APPLICATION NUMBER: PCT/US05/08906
15 <151> PRIOR FILING DATE: 2005-03-17
17 <150> PRIOR APPLICATION NUMBER: US 60/614,817
18 <151> PRIOR FILING DATE: 2004-09-30
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1727
26 <212> TYPE: DNA
27 <213> ORGANISM: homo sapiens
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34 tgcacgtga gcctgcgaaa aagaaggcag aaaagcggct gtttgacgcc tcatccttcg      180
36 ggaaggacct tctggccggc ggagtcgcgg cagctgtgtc caagacagcg gtggcgccca      240
38 tcgagcgggt gaagctgctg ctgcaggtgc aggcgtcgtc gaagcagatc agccccgagg      300
40 cgcggtacaa aggcattggt gactgcctgg tcgcgattcc tcgcgagcag ggtttcttca      360
42 gtttttggcg tggcaatttg gcaaatgtta ttcggtatct tccaacacaa gctctaaact      420
44 ttgcttttaa ggacaaatac aagcagctat tcatgtctgg agttaataaa gaaaaacagt      480
46 tctggagggt gtttttggca aacctggctt ctggtggagc tgctggggca acatccttat      540
48 gtgtagtata tcctctagat tttgcccga cccgattagg tgctgatatt ggaaaaggtc      600
50 ctgaggagcg acaattcaag ggtttagggt actgtattat gaaaatagca aaatcagatg      660
52 gaattgctgg tttataccaa gggtttgggt tttcagtaga gggcatcatt gtgtaccgag      720
54 cctcttattt tggagcttat gacacagtta agggtttatt accaaagcca aagaaaactc      780
56 catttcttgt ctctcttttc attgctcaag ttgtgactac atgctctgga atactttctt      840
58 atccctttga cacagttaga agacgtatga tgatgcagag tggtgagggt aaacggcaat      900
60 ataaaggaac cttagactgc tttgtgaaga tataccaaca tgaaggaatc agttcctttt      960
62 ttctgtggcg cttctccaat gttcttcgcg gtacaggggg tgctttggtg ttggtattat      1020
64 atgataaaat taaagaattc tttcatattg atattggtgg taggtaatcg ggagagtaaa      1080
66 ttaagaaata catggattta acttggttaa catacaaatt acatagctgc catttgcata      1140
68 cattttgata gtgttattgt ctgtattttg ttaaagtgtc agttctgcaa taaagcatat      1200
70 attttttcaa gaatttaaact actaaaaatc agataaatgt ggattttcct ccacttaga      1260
72 ctcaaacaca ttttagtggt atatttcatt tattataggt agtatatttt aatttgtag      1320
74 tttaaaattc tttttatgat taaaaattaa tcatataatc ctagattaat gctgaaatct      1380

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76 aggaaatgaa agtagcgtct tttaaattgc tttcattta atatacctgt tttcccatct 1440
78 tttgaagtca tatggtatga catatttctt aaaagcttat caatagatgt catcatatgt 1500
80 gtaggcagaa ataagctttg ttctatatct cttctaagac agttgttatt actgtgtata 1560
82 atatttacag tatcagcctt tgattataga tgtgatcatt taaaatttga taatgacttt 1620
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104 Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val Lys Leu Leu Leu
105 35 40 45
108 Gln Val Gln Ala Ser Ser Lys Gln Ile Ser Pro Glu Ala Arg Tyr Lys
109 50 55 60
112 Gly Met Val Asp Cys Leu Val Arg Ile Pro Arg Glu Gln Gly Phe Phe
113 65 70 75 80
116 Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg Tyr Phe Pro Thr
117 85 90 95
120 Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys Gln Leu Phe Met
121 100 105 110
124 Ser Gly Val Asn Lys Glu Lys Gln Phe Trp Arg Trp Phe Leu Ala Asn
125 115 120 125
128 Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu Cys Val Val Tyr
129 130 135 140
132 Pro Leu Asp Phe Ala Arg Thr Arg Leu Gly Val Asp Ile Gly Lys Gly
133 145 150 155 160
136 Pro Glu Glu Arg Gln Phe Lys Gly Leu Gly Asp Cys Ile Met Lys Ile
137 165 170 175
140 Ala Lys Ser Asp Gly Ile Ala Gly Leu Tyr Gln Gly Phe Gly Val Ser
141 180 185 190
144 Val Gln Gly Ile Ile Val Tyr Arg Ala Ser Tyr Phe Gly Ala Tyr Asp
145 195 200 205
148 Thr Val Lys Gly Leu Leu Pro Lys Pro Lys Lys Thr Pro Phe Leu Val
149 210 215 220
152 Ser Phe Phe Ile Ala Gln Val Val Thr Thr Cys Ser Gly Ile Leu Ser
153 225 230 235 240
156 Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met Gln Ser Gly Glu
157 245 250 255
160 Ala Lys Arg Gln Tyr Lys Gly Thr Leu Asp Cys Phe Val Lys Ile Tyr
161 260 265 270
164 Gln His Glu Gly Ile Ser Ser Phe Phe Arg Gly Ala Phe Ser Asn Val
165 275 280 285
168 Leu Arg Gly Thr Gly Gly Ala Leu Val Leu Val Leu Tyr Asp Lys Ile
169 290 295 300

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177 <211> LENGTH: 1577
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186 ttctcgaaag acctgctggc cggcgggggtc gcgccgcggg tgtcgaaagc aactgtggcg      180
188 cccatcgagc gtgtgaagct gctgctgcag gtgcaggcgt cctccaagca gataagccct      240
190 gaggcgcgct acaagggcat gctggactgc ctggtgcgca ttcctcgtga gcaaggattt      300
192 ttaagttatt ggcgtggcaa tttggcaaat gttattcgat actttccaac acaagcctta      360
194 aacttcgctt ttaaggacaa atacaaagaa cttttcatgt ctggtgttaa taaagaaaaa      420
196 cagttctgga gatggtttct agcaaacctg gcttctggag gggctgctgg agcaacatcc      480
198 ttgtgtgtag tatacccact agattttgcc agaaccgcat taggtgttga tattggaaaa      540
200 ggtcctgagc agcggcagtt cacgggtttg ggtgactgca ttatgaaaat agccaagtca      600
202 gatggactga ttggtctata ccaaggggtt ggtgtctctg ttcagggtat cattgtttac      660
204 cgagcctctt actttggagc ttatgacacc gttaagggct tattgccaaa gccaaaggaa      720
206 accccatttc ttgtctcttt tatcattgct caaatcgtga ctacctgttc tggaatactc      780
208 tcctatccct ttgacacagt tagaagacgt atgatgatgc agagtgggga atctgatcgg      840
210 caatataaag gaaccataga ctgctttctg aaaatctacc gtcataagg agttcctgcc      900
212 ttcttcctgt gtgccttctc caacatcctt cgtggcacag ggggtgcttt ggtcctgggtg      960
214 ttatatgata aaatcaaaga gttcctcaac attgatgttg gaggtagttc atcaggagat     1020
216 taaattgaga aatgcatatt tctaattgaa aaacatgaaa attacatagc tgccattttt     1080
218 atatattttg atagtgtgtt actactgtca gtgtctctta cagtatttgt tctgcaataa     1140
220 agaaaagatt tttttttcaa gatttttagt ttaaaagtca ggacaaaaat ttttttctact     1200
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224 aaaattctta cacttgtgat gaacaccata taatgtgaaa tatgaggaag tgtctttaaa     1320
226 ctccaatttg cttagtacaa cagtaatccc atcttttagg aattgtattg tatgaccaat     1380
228 agttgaaaag ttgataatga cttagtgaac ctatcaaact atttgaaaag tatagggttg     1440
230 gctattttgct aatgttttagt cttgctagtg tatataaatc tttgaacaag aaatctctgg     1500
232 acattagatt ttgtattctg tatcaataat aaagcaagct caaaactaaa aaaaaaaaaa     1560
234 aaaaaaaaaa aaaaaaa
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 320
239 <212> TYPE: PRT
240 <213> ORGANISM: Mus musculus
242 <400> SEQUENCE: 4
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252 Ala Val Ser Lys Thr Thr Val Ala Pro Ile Glu Arg Val Lys Leu Leu
253          35          40          45
256 Leu Gln Val Gln Ala Ser Ser Lys Gln Ile Ser Pro Glu Ala Arg Tyr
257          50          55          60
260 Lys Gly Met Leu Asp Cys Leu Val Arg Ile Pro Arg Glu Gln Gly Phe
261 65          70          75          80

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264 Leu Ser Tyr Trp Arg Gly Asn Leu Ala Asn Val Ile Arg Tyr Phe Pro
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268 Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys Glu Leu Phe
269           100          105          110
272 Met Ser Gly Val Asn Lys Glu Lys Gln Phe Trp Arg Trp Phe Leu Ala
273           115          120          125
276 Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu Cys Val Val
277           130          135          140
280 Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Gly Val Asp Ile Gly Lys
281 145           150          155          160
284 Gly Pro Glu Gln Arg Gln Phe Thr Gly Leu Gly Asp Cys Ile Met Lys
285           165          170          175
288 Ile Ala Lys Ser Asp Gly Leu Ile Gly Leu Tyr Gln Gly Phe Gly Val
289           180          185          190
292 Ser Val Gln Gly Ile Ile Val Tyr Arg Ala Ser Tyr Phe Gly Ala Tyr
293           195          200          205
296 Asp Thr Val Lys Gly Leu Leu Pro Lys Pro Lys Glu Thr Pro Phe Leu
297           210          215          220
300 Val Ser Phe Ile Ile Ala Gln Ile Val Thr Thr Cys Ser Gly Ile Leu
301 225           230          235          240
304 Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met Gln Ser Gly
305           245          250          255
308 Glu Ser Asp Arg Gln Tyr Lys Gly Thr Ile Asp Cys Phe Leu Lys Ile
309           260          265          270
312 Tyr Arg His Glu Gly Val Pro Ala Phe Phe Arg Gly Ala Phe Ser Asn
313           275          280          285
316 Ile Leu Arg Gly Thr Gly Gly Ala Leu Val Leu Val Leu Tyr Asp Lys
317           290          295          300
320 Ile Lys Glu Phe Leu Asn Ile Asp Val Gly Gly Ser Ser Ser Gly Asp
321 305           310          315          320

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date